

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.**

Application Serial Number: 10/028, 051A  
Source: 1FW16  
Date Processed by STIC: 1/4/05

# ***ENTERED***



IFW16

## RAW SEQUENCE LISTING

DATE: 01/04/2005

PATENT APPLICATION: US/10/028,051A

TIME: 13:03:46

Input Set : A:\NIH133.1CPC1.TXT

Output Set: N:\CRF4\01042005\J028051A.raw

4 <110> APPLICANT: Luyten, Frank P.  
 5 Moos, Malcolm J.R.  
 6 Hoang, Bang  
 7 Wang, Shouwen  
 9 <120> TITLE OF INVENTION: ISOLATION AND USE OF TISSUE  
 10 GROWTH-INDUCING FRZB PROTEIN  
 12 <130> FILE REFERENCE: NIH133.1CPC1  
 14 <140> CURRENT APPLICATION NUMBER: US 10/028051A  
 15 <141> CURRENT FILING DATE: 2001-12-19  
 17 <150> PRIOR APPLICATION NUMBER: US 08/822333  
 18 <151> PRIOR FILING DATE: 1997-03-20  
 20 <150> PRIOR APPLICATION NUMBER: US 08/729,452  
 21 <151> PRIOR FILING DATE: 1996-10-11  
 23 <160> NUMBER OF SEQ ID NOS: 23  
 25 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
 27 <210> SEQ ID NO: 1  
 28 <211> LENGTH: 2374  
 29 <212> TYPE: DNA  
 30 <213> ORGANISM: Bos taurus  
 32 <400> SEQUENCE: 1  
 33 aatagatgcc gcgccccag aagtcttaga cgtcgggaaa gagcagccgg agaggcaggg 60  
 34 gcgcgggcgg ctggcgctcg gcgcagcttt tgggacccca ttgagggaaat ttgatccaag 120  
 35 gaagctgtga gattgccggg ggaggagaag ctccccatc attgtgtcca cttccagggc 180  
 36 ggggaggagg aaacggcgga gcgggcctct cggcgctctc cgcactgctg caccctgccc 240  
 37 catcctgccc agatcatggt ctgcgggagc cgaggcggga tgctgctgct gccggccggg 300  
 38 ctactcgccc tggctgcgct ctgcctgctc cgcgtgcccg gagcgcgggc ggccgcctgt 360  
 39 gagcccgttc gcattcccct gtgcaagtcc ctgccctgga acatgactaa gatgcccac 420  
 40 cacctgcacc acagcaccca ggccaacgcc atcctggcca tcgagcagtt cgaaggctctg 480  
 41 ctgggcaccc actgcagccc ggatctgctc ttcttccctc gtgctatgta cgcgcccac 540  
 42 tgcaccattg acttccagca cgagcccatc aagccctgca agtctgtgtg cgagcggggc 600  
 43 cggcagggct gtgagcccat cctcatcaag taccgccact cgtggccgga aagcctggcc 660  
 44 tgcgaggagc tgccagtata tgaccgcggc gtgtgcatct ctccggaggc catcgctcact 720  
 45 gccgacggag ccgattttcc tatggattcc agtaatggaa actgtagagg agcaagcagt 780  
 46 gaacgctgca aatgtaaacc agtcagagct acacagaaga cctatttccg aaacaattac 840  
 47 aactatgtca ttcgggctaa agttaagaa ataaagacca agtgtcatga tgtgactgca 900  
 48 gtagtggagg tgaaggagat tttaaaggct tctctggtaa acattccaag ggaaactgtg 960  
 49 aacctttata ccagctctgg ctgcctgtgt cctccactta acgttaatga ggagtatctc 1020  
 50 atcatgggct acgaagatga agagcgctcc agattactgt tggtagaagg ttctattgct 1080  
 51 gagaaatgga aggatcgact tggtaaaaaa gttaagcggg gggatatgaa gctccgtcat 1140  
 52 cttggactga atacaagtga ttctagccat agtgattcca ctgagagtca gaagcctggc 1200  
 53 aggaattcta actccgggca agcacgcaac taaatcctga aatgcagaaa atcctcagt 1260  
 54 gacttcctat taagacttgc attgctggac tagcaaaagg aaattgcact attgcacgtc 1320  
 55 atagtctatt ttttagccac aaaaatcagg tggttaactga tattacttct attttttctt 1380

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56 ttgttttctg cttttctcct tccccattc cttttttgt ggtctgagta cagatcctta 1440
57 aatatattat atgtattcta tttcactaat catgggaaaa ctgttctttg caataataat 1500
58 aaattaaaca tgttgatacc agggcctctt tgctggagta aatgttaatt tgctgttctg 1560
59 caccagatt ggggaatgcaa tattggatgc aaagagagat ttctggtata cagagaaagc 1620
60 tagataggct gtaaagcata ctttgctgat ctaattacag cctcattctt gcatgccttt 1680
61 tggcattctc ctcacgctta gaaagttcta aatgtttata aaggtaaaat gacagtttga 1740
62 aatcaaatgc caacaggcag agcaatcaag caccaggaag catttatgaa gaaatgacac 1800
63 atgagatgaa ttatttgcaa gattggcagg aagcaaaata aatagcatta ggagctgggg 1860
64 atagagcatt ttgctgact gagaagcaca actgaagcta gtagctgttg ggggtgttaac 1920
65 agcagcattt ttcttttgac gatacatttg tttgtctgtg aatatattga tcagcattag 1980
66 agcagtggat tgtgaccaga catcaggtgt tatcagcata gctctgttta atttgcttcc 2040
67 ttttagatga acgcattggt gtctttttt tcttctttta aaataaatct cccttgctgc 2100
68 atttgaccag gaaaagaaag catatatgca tgtgcaccgg gctgttattt ttaagatatg 2160
69 tagctctata aaacgctata gtcaaaagat ggtaaaatgt gcaagattct ggggtgtgtg 2220
70 attaattgtg gtgtgtccgc atacactcac actcaagctg aagtgaacga caggcctgtg 2280
71 cactggcctg cactttatca tttggatttg tgctgtttaa tgctcagtaa aatatgctta 2340
72 ataaaaggaa aaaaaaaaaa aaaaaaaaaa aaaa 2374

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74 &lt;210&gt; SEQ ID NO: 2

75 &lt;211&gt; LENGTH: 325

76 &lt;212&gt; TYPE: PRT

77 &lt;213&gt; ORGANISM: Bos taurus

79 &lt;400&gt; SEQUENCE: 2

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80 Met Val Cys Gly Ser Arg Gly Gly Met Leu Leu Leu Pro Ala Gly Leu
81 1 5 10 15
82 Leu Ala Leu Ala Ala Leu Cys Leu Leu Arg Val Pro Gly Ala Arg Ala
83 20 25 30
84 Ala Ala Cys Glu Pro Val Arg Ile Pro Leu Cys Lys Ser Leu Pro Trp
85 35 40 45
86 Asn Met Thr Lys Met Pro Asn His Leu His His Ser Thr Gln Ala Asn
87 50 55 60
88 Ala Ile Leu Ala Ile Glu Gln Phe Glu Gly Leu Leu Gly Thr His Cys
89 65 70 75 80
90 Ser Pro Asp Leu Leu Phe Phe Leu Cys Ala Met Tyr Ala Pro Ile Cys
91 85 90 95
92 Thr Ile Asp Phe Gln His Glu Pro Ile Lys Pro Cys Lys Ser Val Cys
93 100 105 110
94 Glu Arg Ala Arg Gln Gly Cys Glu Pro Ile Leu Ile Lys Tyr Arg His
95 115 120 125
96 Ser Trp Pro Glu Ser Leu Ala Cys Glu Glu Leu Pro Val Tyr Asp Arg
97 130 135 140
98 Gly Val Cys Ile Ser Pro Glu Ala Ile Val Thr Ala Asp Gly Ala Asp
99 145 150 155 160
100 Phe Pro Met Asp Ser Ser Asn Gly Asn Cys Arg Gly Ala Ser Ser Glu
101 165 170 175
102 Arg Cys Lys Cys Lys Pro Val Arg Ala Thr Gln Lys Thr Tyr Phe Arg
103 180 185 190
104 Asn Asn Tyr Asn Tyr Val Ile Arg Ala Lys Val Lys Glu Ile Lys Thr
105 195 200 205
106 Lys Cys His Asp Val Thr Ala Val Val Glu Val Lys Glu Ile Leu Lys

```

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```

107      210      215      220
108 Ala Ser Leu Val Asn Ile Pro Arg Glu Thr Val Asn Leu Tyr Thr Ser
109 225      230      235      240
110 Ser Gly Cys Leu Cys Pro Pro Leu Asn Val Asn Glu Glu Tyr Leu Ile
111      245      250      255
112 Met Gly Tyr Glu Asp Glu Glu Arg Ser Arg Leu Leu Leu Val Glu Gly
113      260      265      270
114 Ser Ile Ala Glu Lys Trp Lys Asp Arg Leu Gly Lys Lys Val Lys Arg
115      275      280      285
116 Trp Asp Met Lys Leu Arg His Leu Gly Leu Asn Thr Ser Asp Ser Ser
117      290      295      300
118 His Ser Asp Ser Thr Gln Ser Gln Lys Pro Gly Arg Asn Ser Asn Ser
119 305      310      315      320
120 Arg Gln Ala Arg Asn
121      325
124 <210> SEQ ID NO: 3
125 <211> LENGTH: 1484
126 <212> TYPE: DNA
127 <213> ORGANISM: Homo sapiens
129 <400> SEQUENCE: 3
130 cggggcctgg gcggsagggg cggtggtctgg agctcggtaa agctcgtggg accccattgg 60
131 ggggaatttga tccaaggaag cggtgattgc cgggggagga gaagctccca gatccttgtg 120
132 tccacttgca gcgggggagg cggagacgcg gagcgggcct tttggcgcc actgcgcggc 180
133 tgcaccctgc cccatcctgc cgggatcatg gtctgcggca gcccgggagg gatgctgctg 240
134 ctgcgggccg ggctgcttgc cctggctgct ctctgcctgc tccgggtgcc cggggctcgg 300
135 gctgcagcct gtgagcccg cgcaccccc ctgtgcaagt ccctgccctg gaacatgact 360
136 aagatgcccc accacctgca ccacagcact caggccaacg ccacccctgg catcgagcag 420
137 ttcgaaggtc tgctgggcac ccactgcagc cccgatctgc tcttcttct ctgtgccatg 480
138 tacgcgcccc tctgcaccat tgacttccag cacgagcccc tcaagccctg taagtctgtg 540
139 tgcgagcggg cccggcaggg ctgtgagccc atactcatca agtaccgcca ctctggtggc 600
140 gagaacctgg cctgcgagga gctgccagtg tacgacaggg gcgtgtgcat ctctcccgag 660
141 gccatcggtta ctgcggacgg agctgatttt cctatggatt ctagtaacgg aaactgtaga 720
142 ggggcaagca gtgaacgctg taaatgtaag cctattagag ctacacagaa gacctatttc 780
143 cggaacaatt acaactatgt cattcgggct aaagttaaag agataaagac taagtgccat 840
144 gatgtgactg cagtagtgga ggtgaaggag attctaaagt cctctctggt aaacattcca 900
145 cgggacactg tcaacctcta taccagctct ggctgcctct gccctccact taatgttaat 960
146 gaggaatata tcatcatggg ctatgaagat gaggaacggt ccagattact cttggtggaa 1020
147 ggctctatag ctgagaagtg gaaggatcga ctcggtaaaa agttaagcg ctgggatatg 1080
148 aagcttcgtc atcttgact cagtaaaagt gattctagca atagtgattc cactcagagt 1140
149 cagaagtctg gcaggaactc gaacccccgg caagcacgca actaaatccc gaaatacaaa 1200
150 aagtaacaca gtggacttcc tattaagact tacttgcaat gctggactag caaaggaaaa 1260
151 ttgcactatt gcacatcata ttctattgtt tactataaaa atcatgtgat aactgattat 1320
152 tactttctgtt tctcttttgg tttctgcttc tctcttctct caaccccttt gtaatggttt 1380
153 gggggcagac tcttaagtat attgtgagtt ttctatttca ctaatcatga gaaaaactgt 1440
154 tcttttgcaa taataataaa ttaaacatgc tgtaaaaaaa aaaa 1484
156 <210> SEQ ID NO: 4
157 <211> LENGTH: 325
158 <212> TYPE: PRT
159 <213> ORGANISM: Homo sapiens

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161 &lt;400&gt; SEQUENCE: 4

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162 Met Val Cys Gly Ser Pro Gly Gly Met Leu Leu Leu Arg Ala Gly Leu
163 1 5 10 15
164 Leu Ala Leu Ala Ala Leu Cys Leu Leu Arg Val Pro Gly Ala Arg Ala
165 20 25 30
166 Ala Ala Cys Glu Pro Val Arg Ile Pro Leu Cys Lys Ser Leu Pro Trp
167 35 40 45
168 Asn Met Thr Lys Met Pro Asn His Leu His His Ser Thr Gln Ala Asn
169 50 55 60
170 Ala Ile Leu Ala Ile Glu Gln Phe Glu Gly Leu Leu Gly Thr His Cys
171 65 70 75 80
172 Ser Pro Asp Leu Leu Phe Phe Leu Cys Ala Met Tyr Ala Pro Ile Cys
173 85 90 95
174 Thr Ile Asp Phe Gln His Glu Pro Ile Lys Pro Cys Lys Ser Val Cys
175 100 105 110
176 Glu Arg Ala Arg Gln Gly Cys Glu Pro Ile Leu Ile Lys Tyr Arg His
177 115 120 125
178 Ser Trp Pro Glu Asn Leu Ala Cys Glu Glu Leu Pro Val Tyr Asp Arg
179 130 135 140
180 Gly Val Cys Ile Ser Pro Glu Ala Ile Val Thr Ala Asp Gly Ala Asp
181 145 150 155 160
182 Phe Pro Met Asp Ser Ser Asn Gly Asn Cys Arg Gly Ala Ser Ser Glu
183 165 170 175
184 Arg Cys Lys Cys Lys Pro Ile Arg Ala Thr Gln Lys Thr Tyr Phe Arg
185 180 185 190
186 Asn Asn Tyr Asn Tyr Val Ile Arg Ala Lys Val Lys Glu Ile Lys Thr
187 195 200 205
188 Lys Cys His Asp Val Thr Ala Val Val Glu Val Lys Glu Ile Leu Lys
189 210 215 220
190 Ser Ser Leu Val Asn Ile Pro Arg Asp Thr Val Asn Leu Tyr Thr Ser
191 225 230 235 240
192 Ser Gly Cys Leu Cys Pro Pro Leu Asn Val Asn Glu Glu Tyr Ile Ile
193 245 250 255
194 Met Gly Tyr Glu Asp Glu Glu Arg Ser Arg Leu Leu Leu Val Glu Gly
195 260 265 270
196 Ser Ile Ala Glu Lys Trp Lys Asp Arg Leu Gly Lys Lys Val Lys Arg
197 275 280 285
198 Trp Asp Met Lys Leu Arg His Leu Gly Leu Ser Lys Ser Asp Ser Ser
199 290 295 300
200 Asn Ser Asp Ser Thr Gln Ser Gln Lys Ser Gly Arg Asn Ser Asn Pro
201 305 310 315 320
202 Arg Gln Ala Arg Asn
203 325

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206 &lt;210&gt; SEQ ID NO: 5

207 &lt;211&gt; LENGTH: 111

208 &lt;212&gt; TYPE: PRT

209 &lt;213&gt; ORGANISM: Rattus norvegicus

211 &lt;400&gt; SEQUENCE: 5

212 Cys Gln Pro Ile Ser Ile Pro Leu Cys Thr Asp Ile Ala Tyr Asn Gln

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Input Set : A:\NIH133.1CPC1.TXT

Output Set: N:\CRF4\01042005\J028051A.raw

```

213 1          5          10          15
214 Thr Ile Met Pro Asn Leu Leu Gly His Thr Asn Gln Glu Asp Ala Gly
215          20          25          30
216 Leu Glu Val His Gln Phe Tyr Pro Leu Val Lys Val Gln Cys Ser Ala
217          35          40          45
218 Glu Leu Lys Phe Phe Leu Cys Ser Met Tyr Ala Pro Val Cys Thr Val
219          50          55          60
220 Leu Glu Gln Ala Leu Pro Pro Cys Arg Ser Leu Cys Glu Arg Ala Gln
221 65          70          75          80
222 Gly Cys Glu Ala Leu Met Asn Lys Phe Gly Phe Gln Trp Pro Asp Thr
223          85          90          95
224 Leu Lys Cys Glu Lys Phe Pro Val His Gly Arg Gly Glu Leu Cys
225          100          105          110
228 <210> SEQ ID NO: 6
229 <211> LENGTH: 111
230 <212> TYPE: PRT
231 <213> ORGANISM: Drosophila melanogaster
233 <400> SEQUENCE: 6
234 Cys Glu Pro Ile Thr Ile Ser Ile Cys Lys Asn Ile Pro Tyr Asn Met
235 1          5          10          15
236 Thr Ile Met Pro Asn Leu Ile Gly His Thr Lys Gln Glu Glu Ala Gly
237          20          25          30
238 Leu Glu Val His Gln Phe Ala Pro Leu Val Lys Ile Gly Cys Ser Asp
239          35          40          45
240 Asp Leu Gln Leu Phe Leu Cys Ser Leu Tyr Val Pro Val Cys Thr Ile
241          50          55          60
242 Leu Glu Arg Pro Ile Pro Pro Cys Arg Ser Leu Cys Glu Ser Ala Arg
243 65          70          75          80
244 Val Cys Glu Lys Leu Met Lys Thr Tyr Asn Phe Asn Trp Pro Glu Asn
245          85          90          95
246 Leu Glu Cys Ser Lys Phe Pro Val His Gly Gly Glu Asp Leu Cys
247          100          105          110
250 <210> SEQ ID NO: 7
251 <211> LENGTH: 319
252 <212> TYPE: PRT
253 <213> ORGANISM: Xenopus laevis
255 <400> SEQUENCE: 7
256 Met Ser Pro Thr Arg Lys Leu Asp Ser Phe Leu Leu Leu Val Ile Pro
257 1          5          10          15
258 Gly Leu Val Leu Leu Leu Leu Pro Asn Ala Tyr Cys Ala Ser Cys Glu
259          20          25          30
260 Pro Val Arg Ile Pro Met Cys Lys Ser Met Pro Trp Asn Met Thr Lys
261          35          40          45
262 Met Pro Asn His Leu His His Ser Thr Gln Ala Asn Ala Ile Leu Ala
263          50          55          60
264 Ile Glu Gln Phe Glu Gly Leu Leu Thr Thr Glu Cys Ser Gln Asp Leu
265 65          70          75          80
266 Leu Phe Phe Leu Cys Ala Met Tyr Ala Pro Ile Cys Thr Ile Asp Phe
267          85          90          95

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RAW SEQUENCE LISTING ERROR SUMMARY  
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:10; N Pos. 21  
Seq#:11; N Pos. 10,16  
Seq#:12; Xaa Pos. 13

## VERIFICATION SUMMARY

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L:372 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!  
L:376 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:10  
L:377 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:0  
L:387 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!  
L:391 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:11  
L:392 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:0  
L:402 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!  
L:406 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:12  
L:407 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:0